

Application No.: 09/745,965

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (currently amended) A computer implemented method for selecting nucleic acid probes comprising:
inputting quality scores and locations for a plurality (n) of candidate probes;
selecting k number of probes from the n number of candidate probes, wherein the selected probes have a maximum aggregate adjusted quality score; wherein the adjusted quality score is based upon the quality score and a penalty for the overlapping of the selected probes; and
outputting the selected probes.
2. (previously presented) The method of Claim 1 wherein the adjusted quality score is calculated according to: $S' = S \sqrt{\frac{l-o}{l}}$, wherein S' is an adjusted quality score; S is the initial quality score; l is the probe length, and o is the overlap the probe has with other probes.
3. (canceled)
4. (previously presented) The method of Claim 2 wherein k is greater than 3.
5. (original) The method of Claim 4 wherein k is greater than 5.

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6. (original) The method of Claim 5 wherein k is greater than 10.
7. (original) The method of Claim 6 wherein k is greater than 15.
8. (previously presented) The method of Claim 2 wherein the selecting step comprises performing dynamic programming optimization on the n number of candidate probes to adjust their quality scores to the extent of overlap between them to obtain an optimal k number of probes with optimal aggregate adjusted quality scores.
9. (previously presented) The method of Claim 8 wherein the selecting comprises steps of:
 - calculating best adjusted quality scores ($Score(i, t)$) for probe i last with $t-1$ probes chosen before i and previous location j providing this best score ($Last(i, k)$);
 - determining the best adjusted quality scores for $Score(j, k)$ to select the last probe; and
 - selecting the next probe according to $Last$ (the probe selected, number of probes remaining to be selected); and
 - repeating the selecting step until all k probes are selected.
10. (currently amended) A system for selecting nucleic acid probes comprising:

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a processor; and

a memory coupled with the processor, the memory storing a plurality of machine instructions that cause the processor to perform logical steps, wherein the logical steps include:

inputting quality scores and locations for a plurality (n) of candidate probes;
selecting k number of probes from the n number of candidate probes, wherein the selected probes have a maximum aggregate adjusted quality score; wherein the adjusted quality score is based upon the quality score and a penalty for the overlapping of the selected probes; and
outputting the selected probes.

11. (original) The system of Claim 10 wherein the adjusted quality score is calculated according to: $S' = S \sqrt{\frac{l-o}{l}}$, wherein S' is an adjusted quality score; S is a quality score; l is the probe length, o is the overlap the probe has with other probes.
12. (canceled)
13. (previously presented) The system of Claim 11 wherein k is greater than 3.
14. (original) The system of Claim 13 wherein k is greater than 5.
15. (original) The system of Claim 14 wherein k is greater than 10.

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16. (original) The system of Claim 15 wherein k is greater than 15.
17. (previously presented) The system of Claim 16 wherein the selecting step comprises performing dynamic programming optimization on the n number of candidate probes to adjust their quality scores to the extent of overlap between them to obtain an optimal k number of probes with optimal aggregate adjusted quality scores.
18. (original) The system of Claim 17 wherein the selecting comprises steps of:
- calculating best adjusted quality scores ($Score(i, t)$) for probe i last with $t-1$ probes chosen before i and previous location j providing this best score ($Last(i, k)$);
 - determining the best adjusted quality scores for $Score(j, k)$ to select the last probe; and
 - selecting the next probe according to $Last$ (the probe selected, number of probes remain to be selected); and
 - repeating the selecting step until all k probes are selected.
19. (currently amended) A computer readable medium having computer executable instructions for performing a method comprising:
- inputting quality scores and locations for a plurality (n) of candidate probes;

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selecting k number of probes from the n number of candidate probes,
wherein the selected probes have a maximum aggregate adjusted quality score;
wherein the adjusted quality score is based upon the quality score and a penalty
for the overlapping of the selected probes; and
outputting the selected probes.

20. (original) The computer readable medium of Claim 19 wherein the adjusted quality score is calculated according to: $S' = S \sqrt{\frac{l-o}{l}}$, wherein S' is an adjusted quality score; S is a quality score; l is the probe length, o is the overlap the probe has with other probes.
21. (canceled)
22. (previously presented) The computer readable medium of Claim 20 wherein k is greater than 3.
23. (original) The computer readable medium of Claim 22 wherein k is greater than 5.
24. (original) The computer readable medium of Claim 23 wherein k is greater than 10.
25. (original) The computer readable medium of Claim 24 wherein k is greater than 15.

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26. (previously presented) The computer readable medium of Claim 25 wherein the selecting step comprises performing dynamic programming optimization on the n number of candidate probes to adjust their quality scores to the extent of overlap between them to obtain an optimal k number of probes with optimal aggregate adjusted quality scores.
27. (original) The computer readable medium of Claim 26 wherein the selecting comprises steps of:
- calculating best adjusted quality scores ($Score(i,t)$) for probe i last with $t-1$ probes chosen before i and previous location j providing this best score ($Last(i,k)$);
 - determining the best adjusted quality scores for $Score(j,k)$ to select the last probe; and
 - selecting the next probe according to $Last$ (the probe selected, number of probes remain to be selected); and
 - repeating the selecting step until all k probes are selected.
28. (new) A computer implemented method for selecting nucleic acid probes comprising:
- inputting quality scores and locations for a plurality (n) of candidate probes;
 - selecting k number of probes from the n number of candidate probes, wherein the selected probes have a maximum aggregate adjusted quality score; wherein the

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adjusted quality score is based upon the quality score and a penalty for the overlapping of the selected probes; and
outputting the selected probes, wherein the outputting of the selected probe sequences is to a file.

29. (new) A system for selecting nucleic acid probes comprising:

a processor; and

a memory coupled with the processor, the memory storing a plurality of machine instructions that cause the processor to perform logical steps, wherein the logical steps include:

inputting quality scores and locations for a plurality (n) of candidate probes;

selecting k number of probes from the n number of candidate probes, wherein the

selected probes have a maximum aggregate adjusted quality score; wherein the

adjusted quality score is based upon the quality score and a penalty for the

overlapping of the selected probes; and

outputting the selected probes, wherein the outputting of the selected probe sequences is to a file.

30. (new) A computer readable medium having computer executable instructions for performing a method comprising:

inputting quality scores and locations for a plurality (n) of candidate probes;

selecting k number of probes from the n number of candidate probes,

wherein the selected probes have a maximum aggregate adjusted quality score;

wherein the adjusted quality score is based upon the quality score and a penalty

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for the overlapping of the selected probes; and
outputting the selected probes, wherein the outputting of the selected probe
sequences is to a file.